

FIGURE 1

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		10	20	30	40	50	60																																																							
RGA5	1	MS	TA	VI	GG	W	FA	Q	S	F	I	Q	T	I	L	L	D	K	A	S	N	C	A	T	O	O	A	R	R	G	I	H	D	D	L	R	R	L	R	T	S	L	R	I	H	A	I	I	D	K	A	E	T	60								
RGA2	1	-M	A	D	V	T	P	Q	A	A	V	F	S	L	V	N	E	I	F	N	R	S	I	N	L	I	V	A	E	R	L	Q	L	N	A	R	A	E	I	N	N	I	Q	R	T	L	L	R	H	S	L	E	E	A	K	A	59					
		70	80	90	100	110	120																																																							
RGA5	61	R	W	N	H	K	N	T	S	L	V	E	I	V	R	O	L	K	D	A	Y	D	A	E	D	L	E	Y	O	A	K	O	V	E	H	R	G	D	O	I	S	D	F	E	S	L	S	T	A	E	W	60										
RGA2	60	R	R	-M	T	D	K	S	L	V	L	W	L	M	E	L	K	E	W	A	Y	D	A	D	D	I	D	D	E	Y	S	A	A	I	R	L	K	V	T	R	—	S	—	T	E	K	R	L	I	D	H	V	I	110								
		130	140	150	160	170	180																																																							
RGA5	121	L	G	A	G	D	D	A	G	T	R	L	R	E	I	O	G	K	L	C	N	I	A	D	M	M	D	V	M	Q	L	A	P	D	G	G	R	O	F	D	W	K	V	V	R	E	T	S	S	E	L	T	E	T	V	V	180					
RGA2	111	T	N	V	P	—	—	L	A	H	K	V	A	D	I	R	K	R	L	N	G	V	T	L	E	R	L	N	I	G	A	L	—	G	S	Q	P	L	D	S	—	T	K	R	G	V	T	T	S	L	L	T	E	S	C	I	163					
		190	200	210	220	230	240																																																							
RGA5	181	F	G	R	D	O	E	R	K	V	V	E	L	L	D	S	G	S	G	N	S	S	F	V	L	P	I	V	G	I	G	K	T	T	L	A	Q	V	Y	N	D	N	R	V	G	N	F	H	L	K	V	W	V	240								
RGA2	164	V	G	R	A	D	K	E	N	L	I	R	L	L	E	P	S	D	G	—	A	V	P	V	P	I	V	G	L	G	A	K	T	T	L	S	O	L	I	F	N	D	K	R	V	E	E	H	F	P	L	R	W	V	221							
		250	260	270	280	290	300																																																							
RGA5	241	C	V	S	D	N	F	N	V	K	R	I	T	K	E	I	E	S	A	T	K	V	E	Q	S	D	K	L	N	L	D	T	L	Q	O	I	L	K	E	K	I	A	S	E	R	F	L	L	V	D	D	V	W	S	E	N	R	D	D	300		
RGA2	222	C	V	S	S	D	D	F	D	V	K	R	I	T	R	E	I	T	E	Y	A	T	I	N	G	R	F	M	D	L	T	N	L	M	L	Q	V	N	L	K	E	E	I	R	G	T	T	F	L	L	V	D	D	V	W	N	E	D	P	V	K	281
		310	320	330	340	350	360																																																							
RGA5	301	W	E	R	L	C	A	P	L	R	F	A	R	G	S	K	V	I	V	T	T	R	D	T	K	I	A	S	T	K	E	I	S	T	E	V	W	E	L	F	K	K	C	A	G	S	V	N	—	359												
RGA2	282	W	E	S	I	L	A	P	L	D	A	G	R	G	S	V	V	I	V	T	T	Q	S	K	V	A	D	V	T	G	T	M	P	V	L	E	L	T	E	D	D	S	W	S	L	E	H	S	F	R	E	A	S	C	341							
		370	380	390	400	410	420																																																							
RGA5	360	P	O	E	H	L	E	V	I	G	R	K	I	A	K	K	I	S	G	L	K	G	S	P	A	A	T	K	V	E	Q	S	D	K	L	N	L	D	T	L	Q	E	H	T	M	E	S	V	W	O	P	A	E	N	I	419						
RGA2	342	S	S	T	N	P	R	M	E	E	I	G	R	K	I	A	K	K	I	S	G	L	K	G	S	P	A	A	T	K	V	E	Q	S	D	K	L	N	L	D	T	L	Q	E	H	T	M	E	S	V	W	O	P	A	401							
		430	440	450	460	470	480																																																							
RGA5	420	F	V	W	L	S	Y	Q	H	P	G	H	L	R	O	C	F	A	C	A	V	E	H	R	D	I	F	K	H	E	I	S	T	E	V	W	E	L	F	K	K	C	A	G	S	V	N	—	479													
RGA2	402	S	A	L	R	R	S	Y	D	N	L	P	O	K	L	C	F	A	C	A	E	T	K	G	R	E	R	K	D	T	L	I	H	M	W	I	A	O	N	L	I	Q	S	T	E	K	R	S	E	M	A	E	C	461								
		490	500	510	520	530	540																																																							
RGA5	480	F	H	E	I	N	R	S	F	F	O	E	S	R	W	R	G	R	Y	V	M	H	E	L	I	D	L	A	Q	F	I	S	V	G	E	C	H	R	I	D	K	S	K	E	T	P	S	T	T	R	I	L	S	V	A	L	T	539				
RGA2	462	F	E	D	D	L	V	C	R	F	F	R	Y	S	—	W	G	N	V	M	N	D	S	V	H	D	L	A	R	W	V	S	L	D	E	F	R	A	D	E	D	S	P	L	H	I	S	K	P	I	R	H	L	S	W	C	S	519				
		550	560	570	580	590	600																																																							
RGA5	540	E	Q	M	K	L	V	D	F	G	Y	N	K	L	T	M	I	N	N	O	N	Q	Y	P	M	T	K	V	N	S	C	L	I	P	H	S	L	F	K	R	L	K	R	I	H	V	L	V	L	O	K	G	M	K	598							
RGA2	520	R	I	T	N	V	L	E	D	N	N	T	G	G	D	A	V	N	P	I	S	L	R	T	L	L	E	G	Q	S	E	F	R	Y	H	L	D	R	M	F	L	M	S	R	I	R	V	L	D	F	S	N	O	V	I	579						

FIGURE 2-1

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	610	620	630	640	650	660	
RGA5	599	ELPDITGDLIQLRYLDISYNACIQRLPESLCDIYNQALRLWGCQLRSFFQGMSKLINLR					658
RGA2	580	NLPSGVNLKHLRYLGLS-NTRIQRLPESVTRICLLQTLLECELCRPLRSMSRLVKLR					638
	670	680	690	700	710	720	
RGA5	659	QLRVEDEIIISKIYEVGKLISLQELSAFKVLNNHGNKIAELSGLTQLRSTLRITNLENVG					718
RGA2	639	OLKANPDVIADIAKVGRILIELQELKAYNVVDKKKGHGIAEELSAMNQLHGDSL1RNQNVEK					698
	730	740	750	760	770	780	
RGA5	719	KEELASKAKLHLRKQYIEALELEWAAGQVSSLEHELLVSEEVILGLOPHFLKSLTIRGYSG					778
RGA2	699	TRESRKARLDEKOKIJKLJDLRWAQCRG--AGECDRDRKVIKGLRPHPNLRELSIKYYGG					755
	790	800	810	820	830	840	
RGA5	779	ATVPSWIDVRLMLPNLGLTILKDENCTREGLSYIYGOLPHLKVLMHKRMPVVKOMSHELCGCT					838
RGA2	756	TSSPSWMTDQYLPNMETIRLRSCHARTELPOLGQLHILRHLHIDGMSQVRQINLOFYGTG					815
	850	860	870	880	890	900	
RGA5	839	KSKLFPRLEELVIEDMPTLKEFPNLALQPLCLKIIMKNMFAVKHIGRELYGDIESNCFLS					898
RGA2	816	EVSGFPLLELNLIRRMPGLEEWS-----EP-----840					
	910	920	930	940	950	960	
RGA5	899	LEELVLQDMLTLEELPNLGQLPHLKVIHMKNMSALKLIGRELCDSEKIKWFPRLEVLVLK					958
RGA2	840	-----R-----RNCCYFPR-----849					
	970	980	990	1000	1010	1020	
RGA5	959	NMIALEELPLSLDNFRVSRRFASSVEVGHGLFSATRNKWFPRLEELIKGMLTFEELHSLE					1018
RGA2	849	-----L-----851					
	1030	1040	1050	1060	1070	1080	
RGA5	1019	KLPCLKVFKRIGLPAVKKIGHGLFDSTCQRECFCPRLEDLVLSDMPAWEWSWAEREELFS					1078
RGA2	851	-----851					
	1090	1100	1110	1120	1130	1140	
RGA5	1079	CLCRILKIEQCPKIKCULLPIPHSLIKLELWQVGLTGLPGLCKGIGGGSSRTASSLHLII					1138
RGA2	851	---KLLIEDCPRLRNLPSPPTLEELRISRTGLVDLPG-FH---GNGDVTNVSLSSLHV-----905					
	1150	1160	1170	1180	1190	1200	
RGA5	1139	KCPNLRLNLGEGLLSNHLPHINAIRIWECAELLWLPVKRFREFTTLENSTIRNCPKLMSMT					1198
RGA2	906	ECRELRLSLSSEGLLQHNLVALKTAAFTDCDSLEFLPAEGFRTAISLPSLIMTNCP---LPC-----963					

FIGURE 2-2

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	1210	1220	1230	1240	1250	1260
RGA5	1199	QCEENDLLEPLTIKALELGDCG---NLGKSLPGCLHNLSSITDIAISNCPYMVSLPREVM				1255
RGA2	963	-----FLLPSSLEHLKLQPCLYPNNNEDSI	STCFENLTSI	SFTD	DIKDCPNLSSFP	PGPL
	1270	1280	1290	1300	1310	1320
RGA5	1256	LHLKELGTIVRTE	ENCDGLGSIEGL	VLKSLKRLAII	IGCPRL	LINE-----GDEQGEVLS
RGA2	1018	COLSALOHLISL	VNCQRLQSIG	EQALTSLES	LTIQNCPRLTMSH	SLVEVNNSSDTGLAFN
	1330	1340	1350	1360	1370	1380
RGA5	1309	ELLELSVDKTI	ALLKLSLIK			
RGA2	1077	ITRWMRRRTGDDG	MLRHRAQND	SFFG	LLQHLT	FLOFLKICQC
	1390	1400	1410	1420	1430	1440
RGA5	1357	LTALRRRLEFFR	OKNLIQSLP	TELH	TPSLHALV	VSDCPQIQSLPEKGLPTLLTDLGFDHCH
RGA2	1137	TSILOILHIVD	DCPNLEVL	PANL	OSLCSL	STLYIVRCPRIHAEP
	1450	1460	1470			
RGA5	1417	PVLT-----	AQLEKHLAEMK	--SSGRFH	PVYA	1441
RGA2	1197	QICQRC	CDPPGGDDWPLT	AN	PRICLGRTH	PCRCSTT

FIGURE 2-3

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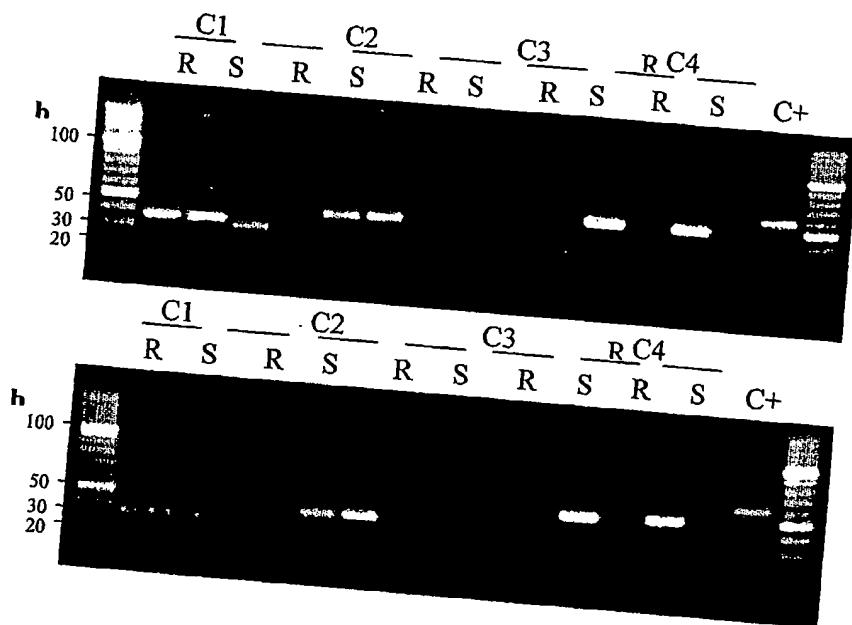


FIGURE 3

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